```
OM of: US-08-711-417C-165 to: Pending_Patents_AA_New:*    out_format : pfs
Date: Aug 28, 2002 10:20 AM
About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/6228611/runat.28082002_100211_13613/app_query.fasta_1.1639
-DB=Pending_Patents_AA_New -QFMT=fastan -SUFFIX=rapn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=6228611_@CGN1_1_56 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-08-711-417C-165
Query length: 1551
Database: Pending_Patents_AA_New
Database sequences: 747981
Database length: 242050750
Search time (sec): 237.910000

score_list:
Sequence                                                Strd Orig   ZScore   EScore  Len  ! Documentation
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-09944-654     + 2551.50 2402.02 5.1e-126  4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-25     + 2467.00 2323.17 1.4e-121  4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-4      + 2458.50 2314.32 3.8e-121 51
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-27     + 2437.00 2294.05 5.0e-120  4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-26     + 2207.50 2078.99 5.3e-108  4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-22     + 1963.00 1849.71 3.4e-95   4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-24     + 1923.50 1812.58 4.0e-93   4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-23     + 1740.00 1642.00 1.6e-83   3
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-28     + 1681.00 1585.31 2.0e-80   3
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-29     + 1625.00 1553.93 1.7e-77   4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-2      + 1360.50 1281.50 1.2e-63 532
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-2      + 1302.00 1226.86 1.4e-60  50
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-3       + 1301.00 1225.92 1.6e-60 507
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-1       + 1282.50 1208.08 1.5e-59 537
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-5       + 1126.00 1061.49 2.4e-51 498
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-31     +  965.50  916.01 6.4e-43   4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-8      +  682.50  651.16 4.0e-28  20
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-37     +  668.50  638.03 2.2e-27   4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-30     +  611.00  582.85 2.2e-24   4
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-36     +  605.00  577.43 4.6e-24   4
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-23913-321     +  395.50  375.87 4.3e-13   4
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-205-823-321     +  395.50  375.87 4.3e-13   4
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-629-469A-14524  +  341.50  324.33 2.9e-10  83
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-629-469A-18929  +  333.50  314.61 7.7e-10   6
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:US-60-389-987-1517    +  333.50  314.61 7.7e-10   6
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:US-60-389-987-527     +  331.50  312.52 9.8e-10   6
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-104-047-2937    +  331.00  310.38 1.0e-09   8
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:US-60-389-987-1850    +  330.00  308.88 1.2e-09   8
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:US-60-389-987-2256    +  313.00  293.90 9.2e-09   5
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-21179-22      +  312.00  293.39 1.0e-08   1
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-629-469A-1947   +  311.00  291.03 1.2e-08  83
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-144-194A-26     +  310.00  291.76 1.3e-08
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-144-194A-98     +  309.50  289.87 1.4e-08   8
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:US-60-389-987-592     +  309.50  289.87 1.4e-08   8
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-09944-733     +  309.00  290.24 1.5e-08   7
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-629-469A-18697  +  308.50  293.40 1.6e-08   4
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-007-280A-231    +  308.00  290.65 1.7e-08
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-21971-13      +  308.00  287.45 1.7e-08
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:US-60-389-987-2498    +  304.50  287.00 2.5e-08  59
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:US-60-389-987-2498    +  303.00  285.17 3.0e-08
/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-10824-201     +  302.00  286.76 3.4e-08
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-629-469A-12631  +  302.00  286.76 3.4e-
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-629-469A-12326  +  302.00  282.55 3.4e-
/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-104-047-3671    +  301.00  288.07 3.9e-08
/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:PCT-US02-09944-654       301.00  278.89 3.9e-08
```

```
seq_name: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-09944-654

seq_documentation_block:
; Sequence 654, Application PC/TUS0209944
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFFO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Darryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHEY, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: DAM, Tam C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEFELD, Yael
; APPLICANT: GERSTIN, JR., Edward H.
; APPLICANT: PERALTA, Careyna H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARWAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael E.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1231 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09944
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/280,068; 60/291,280; 60/291,8
;   60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
;   2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 792
; SOFTWARE: PERL Program
; SEQ ID NO 654
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LI:345320.4.orf2:2001MAY17
PCT-US02-09944-654

alignment_scores:
    Quality:  2551.50          Length:      498
    Ratio:       5.186          Gaps:          3
Percent Similarity:  98.795    Percent Identity:  96.988

alignment_block:
US-08-711-417C-165 x PCT-US02-09944-654
Align seg 1/1  to: PCT-US02-09944-654  from: 1  to: 499

 64 GATACTCCAGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTC 113
    |||||||||||||||||||||||||||||||||||||||||||||||||
```

```
   2 AspThrProAspGluGlyAspGluProMetProIleProGluAspLeuSe  18
 114 CACCACCTCGGAGACAGCAAAGCTCCAAGAGTCGACAGAGTCGTGGCCA  163
     |||||||||||||||||||||||||||||||||||||||||||||||
  18 rThrThrSerGlyGlyGlnGlnSerSerLysSerAspArgValValAlaS  35
 164 GTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAATGGGCGTGCCTGT  213
     ||||||||||||||||||||||||||||||||||||||||||||||||
  35 erAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAlaCys  51
 214 GAAATGAATGGGGAAGAATGTGCCGGAGATTTACGAATGCTTGATGCCTC  263
     ||||||||||||||||||||||||||||||||||||||||||||||
  52 GluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSe  68
 264 GGGAGAGAAAATGAATGGCTCCCACAGGACCAAGGCAGCTCGGCTTTGT  313
     ||||||||||||||||||||||||||||||||||||||||||||
  68 rGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuS  85
 314 CGGGAGTTGGAGGCCATTCGACTTCCTAACGGAAAACTAAAGTGTCATATC  363
     ||||||||||||||||||||||||||||||||||||||||||||||||
  85 erGlyValGlyLyIleArgLeuProAsnGlyLysLeuLysCysAspIle  101
 364 TGTGGGATCATTTGCATCGGCCCAATGTCTCATGGTTCACAAAAGAAG  413
     ||||||||||||||||||||||||||||||||||||||||||||||
 102 CysGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSe  118
 414 CCACACTCGAGAACGGCCCTTCCAGTGCAATCAGTCGCGGGCCTCATTCA  463
     |||||||||||||||||||||||||||||||||||||||||||||
 118 rHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheT  135
 464 CCCAGAAGGGCAACCTGCTCCGCCACATCAAGCTGCATTCCGGGGAGAAG  513
     |||||||||||||||||||||||||||||||||||||||||||||
 135 hrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLys  151
 514 CCCTTCAAATGCCACCTCTGCAACTACGGCTGCCGCCGAGGACGCCCT  563
     |||||||||||||||||||||||||||||||||||||||||||
 152 ProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspAlaLe  168
 564 CACTGGCCACCTGAGGACGCCACCTCCGTTGTAAACCTCACAAATGTGGAT  613
     ||||||||||||||||||||||||||||||||||||||||||||
 168 uThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyT  185
 614 ATTGTGGCCGAAGCTATAAACAGCGAAGCTCTTTAGAGGAACATAAAGAG  663
     |||||||||||||||||||||||:::|||||||||||||||||||
 185 yrCysGlyLysArgSerTyrLysGlnArgSerLeuGluHisLysLysGlu  201
 664 CGCTGCCACAACTACTTGAAAGCATGGGCCTTCCGGGCACACTGTACCC  713
     |||||||||||||||||||||||||||||||||||||||||||||
 202 ArgCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrPr  218
 714 AGTCATTAAAGAAGAAAACTAAGCACAGTGAAATGCAGAAGACCTGTGCA  763
     |||||||||||||:::|||||||||||||||||||||||||||||||
 218 oValIleLysGluGluThrAsnHisSerGluMetAlaGluAspLeuCysL  235
 764 AGATAGGATCAGAGAGATCTCTGCTGCTGGACAGACTAGCAAGTAATGTC  813
     ||||||||||||||||||||||||||||||||||||||||||||||||
 235 ysIleGlySerGluArgSerLeuLeuLeuAspArgLeuAlaSerAsnVal  251
 814 GCCAAACGTAAGACGCTCTATGCCTCAGAAATTTCTTGGGACAAGGGCCT  863
     ||||||||||||||||||||||||||||||||||||||||||||||||
 252 AlaLysArgLysSerMetProGlnLysPheLeuGlyAspLysGlyLyLe  268
 864 GTCCGACACGCCCTACGAC...AGTGCCACGTACGAGAAGGAGAACGAAA  910
     |||||||||||||||||||   |||||:::|||||||||||||||||||
 268 uSerAspThrProTyrAspPheSerAlaSerTyrGluLysGluAsnGluM  285
 911 TGATGAAGTGCCCACGTGATGGACCAAGCCATCAACAACCCCATCAACTAC  960
     ||||||||||||||||||||||||||||||||||||||||||||||||
 285 etMetLysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyr  301
 961 CTGGGGGCCGAGTCCCTGCCCGCCCCTGGTGCAGACGCCCCCGGCGGTTC  1010
     ||||||||||||||||||||||||||||||||||||||||||||||||
 302 LeuGlyAlaGluSerLeuArgProLeuGlnValGlnThrProProGlySe  318
```

```
1011 CGAGGTGGTCCCGGTCATCAGCCGGATGATGTACCAGTCCACAGG...CGCT  1057
     ||||||||||||||||||||||||||||||||||||||||||::: ;
 318 rGluValProValIleSerProMetTyrGlnLeuHisLysProLeuA  335
1058 CGGAGGGCACCCGCGGCTCCACCACTCGGCCAGGACAGCCGCGTGAG  1107
     ::|||||||||||||||||||||||||||||||||||||||||||||
 335 laGluGlyThrProArgSerAsnHisSerAlaGlnAspSerAlaValGlu  351
1108 TACCTGCTGCTGCTCCAAGGCCAAGTTGGTGCCTCCGAGCGCGAGGC  1157
     ||||||||||||||||||||||||||||||||||||||||||||
 352 AsnLeuLeuLeuSerLysAlaLysValProSerGluArgGluAl  368
1158 GTCCCCGAGCAACAGCTGCCAAGACTCCACGACACCGAGAGCAACAACG  1207
     ||||||||||||||||||||||||||||||||||||||||||||||||
 368 aSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsnAsnG  385
1208 AGGAGCAGCCGCAGGCGGTCTTATCTACCTGACCAACCACATCCCCGACGC  1257
     ||||||||||||||||||||||||||||||||||||||||||| :::
 385 luGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIleAlaProHis  401
1258 GCGCAACGC...GTGTCGCTCAAGAGGAGGAGCACCGCGCCTACGACCTGCT  1304
     ||||::::::   :::||||||||||||||||||||||||||||||||||
 402 AlaArgAsnGlyLeuSerLeuLysGluGluHisArgAlaTyrAspLeuLe  418
1305 GCGCGCCGCCTCCGAGAACTCGCAGAGACGCGCTCCGCCGTGGTCAGCACCA  1354
     ||||||||||||||||||||||||||||||||||||||||||||||||
 418 uArgAlaAlaSerGluAsnSerGlnAspSerGlyAlaArgValValSerThrS  435
1355 GCGGGAGCAGATGAAGGTGTACAAGTGCGAACAGTCGCCGGGTGCTCTTC  1404
     |||||||||||||||||||||||||||||||||||||||||||||||
 435 erGlyGluGlnMetLysValTyrLysCysGluHisCysAsnArgValLeuPhe  451
1405 CTGGATCACGTCATGTACACCATCACCATCCACATGGGCTGCCACGGCTTCCGTGA  1454
     ||||||||||||||||||||||||||||||||||||||||||||||||
 452 LeuAspHisValMetTyrThrIleHisMetGlyCysHisGlyPheArgAs  468
1455 TCCTTTTGAGTGCAACATGTGCGGCTACCACAGGGACCCGTACCAGT  1504
     ||||||||||||||||||||||||||||||||||||||||||||
 468 pProPheGluCysAsnMetCysGlyTyrHisSerGlnAspArgTyrGluP  485
1505 TCTCGTGCCACATAACGCGAGGGGAGCACCCGCTTCCACATGAGC  1548
     ||||||||||||||||||||||||||||||||||||||||
 485 heSerSerHisIleThrArgGlyGluHisArgPheHisMetSer  499
```

```
alignment_scores:
        Quality:  2467.00              Length:   461
          Ratio:     5.351                Gaps:     0
Percent Similarity: 100.000   Percent Identity: 100.000
```

```
alignment_block:
US-08-711-417C-165 x US-08-733-622C-25      ..

Align seg 1/1  to: US-08-733-622C-25  from: 1  to: 461

 166 AATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAAATGGCGGTGCCTGTCA 215
     |||||||||||||||||||||||||||||||||||||||||||||||||||
   1 AsnValLysValGluThrGlnSerAspGluGluGluLysTrpArgAlaCysSl 17

 216 AATGAATGGGGAAGAAATGTGCGAGGAGATTTACGAATGCTTGATGCCTCGG 265
     |||||||||||||||||||||||||||||||||||||||||||||||||||
  17 uMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34

 266 GAGAGAAAATGAATGGCTCCCACAGGACCAAGGCAGCTCGGCTTTGTCG 315
     |||||||||||||||||||||||||||||||||||||||||||||||||||
  34 lyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50

 316 GGAGTTGGAGGCATTCGACTTCCTAACCGAAAACTAAAGTGTGATATCTG 365
     |||||||||||||||||||||||||||||||||||||||||||||||||||
  51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67

 366 TGGGATCAATTGCATCGGGCCCAATGTGCTCATGGTTCACAAAAGAAGCC 415
     |||||||||||||||||||||||||||||||||||||||||||||||||||
  67 sGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84

 416 ACACTGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACC 465
     |||||||||||||||||||||||||||||||||||||||||||||||||||
  84 isThrGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100

 466 CAGAAGGCCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCC 515
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 101 GlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysPr 117

 516 CTTCAAATGCCACCTCTGCAACTACGCCTGCCGCCGAGGGACGCCCTCA 565
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 117 oPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspAlaLeuT 134

 566 CTGGCCACCTGAGGACGCACCTCCGTTGGTAAACCTCACAAATGTGATAT 615
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 134 hrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyTyr 150

 616 TGTGGCCCAAGCTATAAACAGCGAAGCTCTTTAGAGGAACATAAAGACG 665
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 151 CysGlyArgSerTyrLysGlnArgThrSerLeuGluGluHisLysGluAr 167

 666 CTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGCACACTGTACCCAG 715
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 167 gCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrProV 184

 716 TCATTAAAGAAGAGAAAACTAAGCACAGTGAAATGGCAGAAGACCTGTGCAAG 765
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 184 alIleLysGluGluThrLysHisSerGluMetAlaGluAspLeuCysLys 200

 766 ATAGGATCAGAGAGATCTCTCGTGCTGGACAGACTAGCAAGTAATGTCGC 815
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 201 IleGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAl 217

 816 CAAACGTAAGACGCTTATGCCTCAGAAAATTTCTTGGGACAAGGGCCTGT 865
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 217 aLysArgLysThrLeuMetProGlnLysIleSerTrpAspLysGlyLeuS 234

 866 CCGACACGCCCTACGACAGTGCCACGTACGAGAGGAGAACGAAATGATG 915
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 234 erAspThrProTyrAspSerAlaThrTyrGluArgArgThrLysMetMet 250

 916 AAGTCCCACGTGATGGACCAAGCCATCAACAACGCCCATCAACTACCTGGG 965
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 251 LysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGl 267

 966 GGCCGAGTCCCTGCGCCCGCTGGTCAGACGCCCCCGGCGGTTCCGAGG 1015
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 267 yAlaGluSerLeuArgProLeuValGlnThrProProGlyGlySerGluV 284
```

```
1016 TGGTCCGGTCATCAGCCCGATGTACCAGCTGCACAGGGGCTCGGAGGGC 1065
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 284 alValProValIleSerProMetTyrGlnLeuHisArgGlySerGluGly 300

1066 ACCCCGCGTCCAACCACTCGGCCCAGGACACAGCCGCGTGGAGTACCTGCT 1115
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 301 ThrProArgSerAsnHisSerAlaGlnAspSerAlaValGluThrLeuLe 317

1116 GCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGGAGGCGCAGGCCTCCCGA 1165
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerProS 334

1166 GCAACAGCTGCCAAGACTCCACGGACACCGAGACCAACAAGGAGGAGCAG 1215
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 334 erAsnSerCysGlnAspSerThrAspThrGluSerAsnAsnGluGluGln 350

1216 CGCCAGCGGTCTTATCTACCTGACCAACCACATCGCCGACGCGCGCAACG 1265
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 351 ArgGlnArgSerTyrLeuProAspGlnHisIleAlaArgArgAlaGlnAr 367

1266 CGTGTCGCTCAAGGAGGAGCACCGCGCTACGACCTGCTGCGCGCCCCCT 1315
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 367 gValSerLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAlaS 384

1316 CCGAGAACTCGCAGGACGACGCTCCGGTGGTCAGCACCAGCGGGAGCAG 1365
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 384 erGluAsnSerGlnAspAspAlaLeuArgValValSerThrSerGlyGluGln 400

1366 ATGAAGTGTACAAGTGCGAACACTGGCCGCGGGTGCTCTTCCTGGATCACGT 1415
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 401 MetLysValTyrLysCysGluHisCysArgValLeuPheLeuAspPHisVa 417

1416 CATGTACCACCATCCACATGGGCTGCCACGGCTTCCGTGATCCTTTGAGT 1465
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 417 lMetTyrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluC 434

1466 GCAACATGTGCGCTACCACAGCGCAGGACCGGTACGAGTTCTCGTCGCAC 1515
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 434 ysAsnMetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHis 450

1516 ATAACGCGAGGGAGCACCGCTTCCACATGAGC 1548
     ||||||||||||||||||||||||||||||||
 451 IleThrArgGlyGluHisArgPheHisMetSer 461
```

```
alignment_scores:
      Quality:  2458.50              Length:      518
        Ratio:  4.947                  Gaps:        5
Percent Similarity: 95.946      Percent Identity: 90.347

alignment_block:
```

Wed Aug 28 10:05:41 2002

us-08-711-417c-165.rapn

```
US-08-711-417C-165 x US-10-037-667-4

Align seq 1/1  to: US-10-037-667-4   from: 1  to: 515

1    ATGGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGAGGAAAG      50
     ||||||::::||||||||||||||||||||
1    MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe  17

51   CCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC   100
     ||||||||||||||
17   rProProValSerAspThrProAspGluGlyAspGluProMetProValP  34

101  CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAGAGTGAC  150
     ||||||||||||||:::|||||||
34   roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp  50

151  AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA  200
     |||  ::||||||||||||||||
51   ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs  67

201  TGGGCGTGCCTGTGAAATGAATGGGGAAGAAATGTGCGGAGGATTTACGAA 250
     ||||||||||||||
67   nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM  84

251  TGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCACAGGACCAAGGC    300
     ||||||||||||||
84   etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100

301  AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGAAAACT   350
     ||||||||||||||
101  SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117

351  AAAGTTGATATCTGTGGGATCATTGCATCGGCCCAATGTGCTCATGG    400
     ||||||:::||||||
117  uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134

401  TTCACAAAAGAGCCACACTGGAGACGGCCCTTCCAGTGCAATCAGTGC    450
     ||||||||||||||
134  alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnCys 150

451  GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA  500
     ||||||||||||||
151  GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167

501  TTCCGGGAGAGCCCTCAAATGCCACCCTGCCACCTACGCCTGCCGCC    550
     ||||||||||||||
167  sSerGlyLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA    184

551  GGAGGACGACCCCTCACTGGCCACCTGAGGACGGCACTCCGTTGGTAAACCT 600
     ||||||||||||||
184  rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200

601  CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAAGCTCTTTAGA  650
     |||||||||||::::|||||||
201  HisLysCysGlyTyrCysGlyLysAlaSerTyrLysGlnArgSerLeuGl 217

651  GGAACATAAAGAGCGCGCTGCCACAACTACTTGGAAAGCCATGGGCCTTCCGG 700
     ||||||||||||||
217  uGluHisLysGluArgCysHisAlaTyrLeuGluSerMetGlyLeuProG 234

701  GCACACTGTACCCAGTCATTAAAGAAGAAAAACTAAGCACAGTGAAATGGCA 750
     ||  ::: |||||||||
234  ly...ValCysProValIleLysGluGluThrAsnHisAsnGluMetAla 249

751  GAAGACCGTGCAAGATAGGATCAGAGAGATCTCTCGTTCGTCTGGACAGACT 800
     |||||||::::|||||||||
250  GluAspLeuCysLysIleGlyAlaGluSerLeuValLeuAspArgArgLe 266

801  AGCAAGTAATGTCCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850
     |||||||||:::||||||
266  uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 283

851  GGGACAAGGGCCTGTCCGACACGCCGTCTACGACAGTGCCCACGTACGAGAAG 900


283  lyAspLysCysLeuSerAspMetProTyrAspPheSerAlaAsnTyrGluLys 299

901  GAGAACGAAATGATGAAGTCCCACGTGATGACCAAGCCATCAACAACGC   950
     || ::|||||||||||||||
300  Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 315

951  CATCAACTACCTGGGGCCGAGTCCCTGCGCCCGCTGGTGCAGACGCCCC  1000
     ||||||||||||||
315  aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 332

1001 CGGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC 1050
     ||||||::::|||||||
332  roGlySerSerGlyValValProValIleSerProMetTyrGlnLeuHis 348

1051 AGG...CGCTCGGAGGGCACCCGCGTCCAACCACTCGGCCCAGGACAG   1097
     |||::::||| ||||||||||||
349  LysProProSerArgGlyProProArgSerAsnHisSerAlaGlnAsp.. 364

1098 CGCCGTGAGTACCTGCTGCTGCTCCAAGGCCAAGTTGGTGCCCTCGG    1147
     ||||||||||||||
365  .AlaValAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerSerG 381

1148 AGGCGGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
     ||||||||||||||
381  luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397

1198 AGCAACAACGAGGAGCAGCGCAGCGGTCTTATCTACCTGACCAACCCAT  1247
     ||||||||||||||
398  SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIl 414

1248 CGCCCGACGCGCCGCCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT 1294
     |||| ::::|||||||||||
414  eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnGlnArgAlaT 431

1295 ACGACCTGCTGCGCGCGCCTCCGAGAACTCGCAGGACGCCGGTCCGCGTG 1344
     ||::::|||||||||||||:::|||
431  yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 447

1345 GTCAGCACCAGCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394
     ||||||||||||||
448  ValSerThrSerGlyGluGlnMetLysValTyrLysCysGluHisCysAr 464

1395 GGTGTCTTCCTGGATCACGTCATCGTCATGTACACCATCCACATGGGCTGCCACG 1444
     ||||||||||||||
464  gValLeuPheLeuAspHisValValMetTyrThrIleHisMetGlyCysHisG 481

1445 GCTTCCGTGATCCTTTGAGTGCAACATGTGCGGCTACCAGCCAGGAC    1494
     ||||||||||||||
481  lyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 497

1495 CGGTACGAGTTCTGTGCCACATAACGGCGAGGGGAGCACCGCTTCCACAT 1544
     |||||||||||::::|||
498  ArgTyrGluPheSerHisIleThrArgGlyLeuHisArgTyrHisSerLe 514

1545 GAGC 1548
     :|||
514  uSer 515
```

```
;   PRIOR FILING DATE: 1995-10-18
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 27
;   LENGTH: 518
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-08-733-622c-27

alignment_scores:
         Quality:  2437.00          Length:    521
           Ratio:     4.913            Gaps:      6
Percent Similarity:  95.202   Percent Identity:  89.635

alignment_block:
US-08-711-417C-165 x US-08-733-622c-27

Align seg 1/1   to: US-08-733-622C-27   from: 1  to: 518


  1 ATGGATGCTGACGAGGTCAAGACATGTCTTCTTCATCAGGAAGGAAAG   50
    ||||||.:||||||||||||||||||||||||||||||||||||||||
  1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe   17

 51 CCCCCCTGTAAGCGATATCTCCAGATGAGGGGCGATGAGCCCATGCCGATCC  100
    ||||||||||||||||||||||||||||||||||||||||:::|
 17 rProProValSerAspThrProAspGluArgGlyAspGluProMetProValP   34

101 CCGAGGACCCTCCACCACCTCGGGAGGACAGCAGCAAAGCTCCAAGAGTGAC  150
    |||||||||||||||||:||||||:::::||||||||||
 34 rGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp   50

151 AGAGTCGTGGCCAGTAATGTTAAAGTAGGACTCAGAGTGATGAAGAAGAA  200
    |||  .:||||||||||||||||||||||||||||||||||||||
 51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerGluAspGluAs   67

201 TGGGCGTGCCTGTGAAATGAATGAATGGGGAAGAATGTGCGGAGGATTTACGAA  250
    |||||||||||||||||||||||||||||||||||||||||||||||||
 67 nGlyArgAlaCysGluMetAsnGlyGluGluValGlyLysAlaGluAspLeuArgM   84

251 TGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCCAGGGACCAAGGC  300
    |||||||||||||||||||||||||||:||||||||||||||
 84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisGlyArgGlnGly  100

301 AGCTCGGCCTTTGTCGGGAGTTGAGGCATTCGACTTCCTAACGGAAAACT  350
    |||||||||||||||||||||||||||||||||||||||||||||||
101 SerSerAlaLeuSerGlyValGlyGlyIleGlyArgLeuProAsnGlyLysLe  117

351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCCAAATGTGCTCATGG  400
    |||||||||||||||||:||||||||||||||||||||||||||||
117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV  134

401 TTCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC  450
    |||||||||||||||||||||||||||||||||||||||||
134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer  150

451 GGGGCCTCATTCACCCAGAAGGGCAACCTGCTTCCGGCAACAATCAAGCTGCA  500
    |||||||||||||||||||||||||||||||||||||||||
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysSerLeuHi  167

501 TTCCGGGGAGAAGCCCTTCAAATGCCAACTCTGCAACTACCCCTGCCGCC  550
    |||||||||:::|||||||||||||||||||||||||||||||||||||
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA  184

551 GGAGGGACGCCCTCACTGGCCACCTCGAGGACGCACTCCGTTGGTAAACCT  600
    ||||||||||||||||||||||||||||||||||||||||:::|||||
184 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro  200

601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGGCAACGTCTTTAGA  650
    ||||||||||||||||:||||||||||||||:::||||||||||
201 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnAlaThrArgSerLeuGl  217

651 GGAACATAAAGAGCCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG  700
```

```
    |||||||||||||||||||||||||||||||||||||||||||||||||
217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG   234

701 GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCA   750
    ||| ::::|||||||||||||||||||||||||||||||||||
234 ly...ValCysProValIleLysGluGluThrLysHisSerGluMetAla   249

751 GAAGACCTGTGCAAGATAGGATCAGAGAGAGATCTTCGTGCTGCAGACT   800
    ||||||||||||||||||||||:|||||||||||||||||||||||
250 GluAspLeuCysLysIleGlyAlaGlyArgAspLeuArgAlaAspArgLe   266

801 AGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG   850
    |||||||||||||||||||||||||||||||||||:|||||||||||
266 uAlaSerAsnValAlaLysSerMetProGlnLysPheLeuG   283

851 GGGACAAGGGCCTGTCCACACGCCCTACGACGTGCCACGTACGAGAAG   900
    ||||||||    ||||||||||||||||:||||||||||||||
283 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys   299

901 GAGAACGAAATGATGAAGTCCCACGTGATGACCAAGCCATCAACAACGC   950
    |||||||   ||||||::|||||||||||||||||||||||
300 Glu...AspMetThrSerHisValMetAspGlnAlaIleAsnAsnAl   315

951 CATCAACTACCTGGGGGCCGAGTCCCTGCGCCCCGTGGTGCAGACGCCCC  1000
    ||||||||||||||||||||||||||||||||:||
315 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP   332

1001 CGGGGGGTTCCGAGGTGGTCCCGGTCATCACCCCGATGTACCAGCTGCAC  1050
    |||||||||||||:|||||||||||||||||||||||
332 roGlySerGluValProValIleSerSerMetTyrGlnLeuHis   348

1051 AGG...CGCTGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACAG  1097
    :::   ||||||:|||||||||||||||||||||||||
349 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnHisAsp..   364

1098 CGCCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG  1147
    |||||||:   :||||||||||||||||||
365 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG   381

1148 AGGCGGAGGGCTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG  1197
    ||||||||||||||||||||||||||||||||||||||
381 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu   397

1198 AGCAACAACGAGGACGAGCAGCCCAGCGGTCTTATCTACCTGACCAACCACAT  1247
    |||||     ||:|||||||||||||||||||||||||||||
398 SerAsnAlaGluGluGluGlnGlyLeuIleTyrLeuThrAsnHisIl   414

1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT  1294
    :::::|||::   .:::::::|||||||||:|||||
414 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAlaT   431

1295 ACGACCTGCTGCGCGCCCTCCGAGAACTGCCGAGACGACGCCGCTCCGCGTG  1344
    |||::::||||||||||||||||||||:::|||||
431 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal   447

1345 GTCAGCACCAGCGGGAGCAGATGAAGTGCGAACACTGCCG  1394
    ||||    |||||||||||:||||||||||||||||||
448 ValSerThrSerGlyGlnLeuLysValTyrLysCysGluHisCysSerAr   464

1395 GGTGCTCTTCCTGGATCACGTCATGTACCATCACATG........G  1435
    :::::::|||   .::::::|||||||||||||||
464 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG   481

1436 GCTGCCACGGCTTCCGTGATCCTTTGAGTGCCAACATGTGCGGCTACCAC  1485
    |:::::||||||||||||||||||||||||:::||||
481 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis   497

1486 AGCCAGGACCCGTACGAGTTCTGTCGCACATAACCGCGAGGGAGCACCG  1535
    |||||||||||||||||||||||||||||||||||
498 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr   514

1536 CTTCCACATGAGC  1548
    :::::||::|||
```

```
     514 gTyrHisLeuSer 518

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-22

seq_documentation_block:
; Sequence 22, Application US/08733622C
; GENERAL INFORMATION:
;   APPLICANT: Georgopoulos, Katia
;   APPLICANT: Morgan, Bruce A.
;   TITLE OF INVENTION: AIOLOS GENE
;   FILE REFERENCE: 10287-030001
;   CURRENT APPLICATION NUMBER: US/08/733,622C
;   CURRENT FILING DATE: 1996-10-17
;   PRIOR APPLICATION NUMBER: US 60/017,646
;   PRIOR FILING DATE: 1996-05-14
;   PRIOR APPLICATION NUMBER: US 60/005,529
;   PRIOR FILING DATE: 1995-10-18
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: majority sequence
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(470)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-08-733-622C-22

alignment_scores:
         Quality:  2207.50         Length:     468
         Ratio:       5.098          Gaps:        3
Percent Similarity:  92.521    Percent Identity:  90.385

alignment_block:
US-08-711-417C-165 x US-08-733-622C-22    ..

Align seg 1/1  to: US-08-733-622C-22  from: 1 to: 470
```

```
1445 GCTTCCGTGATCCTTTGAGTGCAACATGTGCGGCTACCACAGCCAGGAC 1494
     |||||||||||||||||||||||||||||||||||||||||||||||||
 436 lyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452

1495 CGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAGCACCGCTTCCACAT 1544
     ||||||||||||||||||||||||||||||||||||||||  |||
 453 ArgTyrGluPheSerHisIleThrArgGlyGluHisArg***His** 469

1545 GAGC 1548
     |||
 469 *Ser 470 .
```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-26

```
alignment_scores:
        Quality: 1963.00          Length:      521
          Ratio:    4.776            Gaps:        6
Percent Similarity:  78.887     Percent Identity: 74.280

alignment_block:
US-08-711-417C-165 x US-08-733-622C-26  .

Align seg 1/1 to: US-08-733-622C-26  from: 1  to: 432

  1 ATGGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGGAGGAAGAAAG  50
    ||||:||:||||||||||||||||||||||||||     |||||||||||||
  1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe  17

 51 CCCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC  100
    ||||||||  |||||||||||||||||||||||||||||||:||:|||
 17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP  34

101 CCGAGGACCCTCCACCACCTCCGGAGGACGAGCAGCAAAGCTCCAAGAGTGAC  150
    ||||||:||:|||||||||||||||||||||:|||||:::||||||||||
 34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp  50

151 AGAGTCGTGGCCAGTAAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA  200
    |||  ::|||||||||||||||||||||||||||||||||||||||||
 51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerGluGluGluAs  67

201 TGGGCGTGCCTGTGAAAATGAAATGGGGAAGAAATGTGCGGAGGATTTACGAA  250
    ||||||||||||| |||||||||||||||||||||||||||||||||||
 67 nGlyArgAlaCysGlumetCysAsnGlyGlyLysCysAlaGluAspLeuArgM  84

251 TGCTTGATGCCTCCGGAGAGAAAATGAATGAATGGCTCCCACAGGACCAAGGC  300
    ||||||:||||||||||||||||||||||||||||||||||||||||||||
 84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly  100

301 AGCTCGGCTTTGTCGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT  350
    ||||||||||||||||||||||||||||||||||||||||||||||||
101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuLeuThrAsnHisIl  117
```

```
351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGCCCCAAATGTGCTCATGG  400
    ||||||||||||||||||||||||||::|||||||||||||||||||||
117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV  134

401 TTCACAAAAGACCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC  450
    |||||||||||||||||||||||||||||||||||    |||
134 alHisLysArgSerHisThrGlyAlaArgProPheGlnCysAsnGlnSer  150

451 GGGGCCTCATTCACCCAGGAGGGCAAACTGCTCCGGCACATCAAGCTGCA  500
    ||||||||||||||||||||||||||||||||||||||||||||||||
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi  167

501 TTCCGGGGAGAGCCCTTCAAATGCCACCTCTGCAACTACGCCTGCCGCC  550
    ||||||||||||||||||||||||||||||||||||||||||||||||
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA  184

551 GGAGGGACCGCCCTCACTGCCGCCACCTGAGGACGCCACTCCGTTGGTAAACCT  600
    |||||||||||||||||||||||||||||||||||||||||
184 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSer............  196

601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA  650
    ...............................................
196 ..................................................  196

651 GGAACATAAAGAGCCGTGCCACAACTACTTGGAAAGCATGGCCGCCTTCCGG  700
    .................................................
196 ..................................................  196

701 GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACACAGTGAAATGGCA  750
    .................................................
196 ..................................................  196

751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTGCTGGACAGACT  800
    ..................................................
196 ..................................................  196

801 AGCAAGTAATGTCGCCAAACGTAAGAGCTTCATGCCTCAGAAATTTCTTG  850
    .................................................
197 ...........................................G  197

851 GGGACAAGGGCCTGTCGACAGCGCCACTACGACGTGCCACGTACGAGAAG  900
    ||||||  |||||||    |||||||||||||||||:::||||||||||
197 lyAspIysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys  213

901 GAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGC  950
    ||||||||  ::||||||||||||||||||||||||||||||||||||||
214 Glu...AspMetThrSerHisValMetAspGlnAlaIleAsnAsnAl  229

951 CATCAACTACCTGGGGGCCGAGTCCCTGCGCCCCGTGGTGCAGAGCGCCCC  1000
    |||||||||||||||||||||||||||||||||||||||:||||||
229 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP  246

1001 CGGGCGGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC  1050
     ||||:::|||||||||||||||||||||||||      |||||||||||
246 roGlySerSerGluValProValIleSerSerMetTyrGlnLeuHis  262

1051 AGG...CGCTCGAGGGGCACCCGCGCTCCAACCACTCGGCCCAGGACAG  1097
     ||:    :::|||||:|||||||||||||||||||||||||||||||||
263 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp..  278

1098 CGCCCTGGGATACCTGCTCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG  1147
     |||||:    ||||| |||| |||||||||||||||||||||||||||||
279 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG  295

1148 AGCCGCGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG  1197
     ||||||||||:||||||||||||||||||||||||||||||||||||||
295 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu  311

1198 AGCAACAACGAGGAGCAGCGCAGCGGTCTTATCTACCTGACCAACCACAT  1247
     ||||||||||||||||||||||||||||||||||||||||||||||||
312 SerAsnAlaGluGluGlnArgSerGlyIleTyrLeuThrAsnHisIl  328
```

us-08-711-417c-165.rapn

```
1248 CGCCCACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCACCCGCGCCCT 1294
     |         ::::||||| :::::||||||||||||::::||||||||
 328 eAsnProHisAlaArgArgAsnGlyLeuAlaLeuLysGluGlnArgAlaT 345

1295 ACGACCTGCTGCGCGCGCCTCCGAGAACTGCGAGACGCGCCTCCGCGTG 1344
     ||::::||||||||||||||||||||||||||||||||||:::||||||
 345 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 361

1345 GTCAGGACCAGCGGGAGCAGATGAGAGGTGTACAAGTGCCAACACTGCCG 1394
     ||||||||||||||||||||||||||||||||||||||::||||||||||
 362 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGlnHisCysAr 378

1395 GGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATG.........G 1435
     |||||||||||||||||||||||||||||||||||||||          |
 378 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 395

1436 GCTGCCACGGCTTCCGTGATCCTTTCAGTGCAACATGTGCGGCTACCAC 1485
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 395 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 411

1486 AGCCAGGACCGGTACAGAGTTCTCGTCGCACATAACCGCGAGGGAGCACCG 1535
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 412 SerGlnAspArgTyrGlyPheSerSerHisIleThrArgGlyGluHisAr 428

1536 CTTCCACATGAGC 1548
     |:::||||::|||
 428 gTyrHisLeuSer 432
```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-24

seq_documentation_block:
; Sequence 24, Application US/08733622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; CURRENT FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-733-622C-24

alignment_scores:
               Quality: 1923.50   Length: 521
               Ratio: 4.703   Gaps: 7
Percent Similarity: 78.503   Percent Identity: 73.129

alignment_block:
US-08-711-417C-165 x US-08-733-622C-24

Align seg 1/1 to: US-08-733-622C-24 from: 1 to: 431

```
   1 ATGGATGCTGACGAGGTCAAGACATGTCTTTCATCAGGGAGGAAAG 50
     | ||||||||||||||::||||||||||||||||||||||||||||
   1 MetAspValAlaAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17

  51 CCCCCCTGTAAGCAATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC 100
     ||||||||||||||||||||||||||||||||||||||||||:::|||||
  17 rProProValSerAspThrProAspGluGlyAspGlyAspProMetProValP 34

 101 CGGGCGGTTCCGAGGTGTCCCGGTCATCACGCCGATCTACCAGTCGCAC 150
     ||||||||||||||||||||||||||||||||:::||||||||||||||
  34 roGlySerSerGlyValProValIleSerSerMetTyrGlnLeuHis 50
```

```
151 AGAGTCGTGGCCAGTAAGTGTTAAAGTAGAGACTCAGAGTGATGATGAAGAGAA 200
    |||       ::|
 51 ArgGlyMet. 53

201 TGGGCGTGCCTGTGAAATGAATGGGAGAGAATGTGCGGAGGATTTACGAA 250
    ............
 53 .......... 53

251 TGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCACAGGGACCCAAGGC 300
    ............
 53 .......... 53

301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTGGACTTCCTAACGGAAAACT 350
    ...............
 53 .......... 53

351 AAAGTGTGATATCTGTGGATCATTTGCATCGGGCCCAATGTGCTCATGG 400
    ...............
 53 .......... 53

401 TTCACAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC 450
    |||||||||||||||||||||||||||||||||||||||
 54 .....GlyGluArgProPheGlnCysAsnGlnSer 63

451 GGGGCCTCATTCACCCAGAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 64 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 80

501 TTCCGGGGAGAGCCCTCAAATGCCACCTGCAACTACGCCCTGCCGCC 550
    ||||||||||||||||||||||||||||||||||||||||||||||||
 80 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 97

551 GGAGGGACGGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 97 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 113

601 CACAAATGTGGATAATTGTGGCCGAAGCTATAAACACGCGAACGTCTTTAGA 650
    ||||||||||||||||||||||||||||||::||||||||
114 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuGl 130

651 GGAACATAAAGAGCGCTGCCACCAACTACTTGGAAAGCATGGGCCTTCCGG 700
    |||||||||||||||||||||||||||||||||||||||||||||
130 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 147

701 GCACACTGTACCCAGTCATTAAAGAAGAAGAAACTAAGCACAGTGAAATGGCA 750
    ||       ::  |||||||||||||||||:::||||||||
147 ly...ValCysProValIleLysGluGluThrAsnHisAsnGluMetAla 162

751 GAAGACCGTGCAAGATAGGATCAGAGAGATCTCTGCTGCGACAGACT 800
    |||||||||||||||:::|||||||||||||||||||||||||
163 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 179

801 AGCAAGTAATGTCGCCAAAACGTAAGAGCTCTATGCCCTCAGAAATTCTTG 850
    |||||||||||||||||||||||||||||||||||||||||||||
179 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 196

851 GGGACAAGGGCCTGTCCGACACCCCTACGACGACTACGAGAAG 900
    |||||||||||||||||||||||||||||||||||||
196 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 212

901 GAGAACGAAATGATGAAGTCCCACGTGATGACCAAGCCATCAACAACGC 950
    |||   :::|||   ||||||||||||||||||||||||||||||
213 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 228

951 CATCAACTACCTGGGGCCGAGTCCCTGCGCCCGCTGTGCAGACGCCCC 1000
    ||||||||||||||||||||||||||||||||||||||||||||||||
228 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 245

1001 CGGGCGGTTCCGAGGTGTCCCGGTCATCACGCCGATCTACCAGTCGCAC 1050
     ||||||||||||||||||||||||||||||||||||||||||
245 roGlySerSerGlyValProValIleSerSerMetTyrGlnLeuHis 261
```

us-08-711-417c-165.rapn

Wed Aug 28 10:05:41 2002

```
alignment_block:
US-08-711-417C-165 x US-08-733-622C-23    ..

Align seq 1/1  to: US-08-733-622C-23   from: 1  to: 334

  421 GGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGCCTCATTCACCCAGAA 470
      |||||||||||||:::||||||| |||||||||||||||||||||||||
    1 GlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThrGlnLy 17

  471 GGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCA 520
      |||||||||||||||||||||||||||||||:|||||||||||||||:||
   17 sGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysProPheL 34

  521 AATGCCACCTGCTCAACTACGCCTGCGCCGGAGGGACGGCCCTCACTGGC 570
      ||||||  |||||||||||||||||||||||||||||||||||||||||
   34 ysCysHisLeuCysAsnTyrAlaCysArgArgArgAspAlaLeuThrGly 50

  571 CACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATGTGATATTGTGG 620
      | ::::|||||||||||||||||||||||||||||||||||........
   51 HisLeuArgThrHisSer...............                56

  621 CCGAAGCTATAAACAGCGAACGTCTTTAGGAGAACATAAAGAGCGCTGCC 670
      ||:::||::||||||||||||||||:::||||||||||||:||||:|||||
   56 ...............                                  56

  671 ACAACTACTTGGAAAGCATGGCCCTTCCGGGCACACTGTACCCAGTCATT 720
      |||:::||||||||||||||:::|||||||||||||||||||||||||||
   57 ...............ValIle                            58

  721 AAAGAGAAACTAAGCACAGTGAAATGCAGAAGACCTGTCAAGATAGG 770
      ||||||||||||||||||||||||||||||||||||||||||||||||
   59 LysGluGluThrLysHisSerGluMetAlaGluAspLeuCysLysIleGl 75

  771 ATCAGAGAGATCTCTGTGCTGGACAGACTAGCAAGTAATGTCGCCAAAC 820
      |||||||||||||||||||||||||||||||||||||||||||||||||
   75 ySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAlaLysA 92

  821 GTAAGAGCTCTATGCCTCAGAAATTTCTTGGGACAAAGGGCCGTCTCCGAC 870
      |||||||||||||||||||||||||||||||||||||||||||||||||
   92 rgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeuSerAsp 108

  871 ACGCCCTACGACAGTGCCACGTACGAGAAGGAGAACGAAATGATGAAGTC 920
      |||||||||||||||||||||||||||||||||||||||||||||||||
  109 ThrProTyrAspSerAlaThrTyrGluLysGluAsnGluMetMetLysSe 125

  921 CCACGTGATGGACCAAGCCATCAACAACGCCATCAACTACCTGGGGCCG 970
      |||||||||||||||||||||||||||||||||||||||||||||||||
  125 rHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGlyAlaG 142

  971 AGTCCCTGCGCCGGCTGGTGCAGACCGCCCCCGGCGGTTCGAGGTGGTC 1020
      |||||||||||||||||||||||||||||||||||||||||||||||||
  142 luSerLeuArgProLeuValGlnThrProProGlyGlySerGluValVal 158

 1021 CCGGTCATCAGCCGATGTACCAGTCTGCACAGGCGTCGGAGGGCACCCC 1070
      |||||||||||||||||||||||||||||||||||||||||||||||||
  159 ProValIleSerProMetTyrGlnLeuHisArgArgSerGluGlyThrPr 175

 1071 GCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGAGTACCTGCTGTGC 1120
      |||||||||||||||||||||||||||||||||||||||||||||||||
  175 oArgSerAsnHisSerAlaGlnAspSerAlaValGluTyrLeuLeuLeuL 192

 1121 TCTCCAAGGCCAAGTTGGTGCCCTCGGACGCGGAGGCGTCCCCGAGCAAC 1170
      |||||||||||||||||||||||||||||||||||||||||||||||||
  192 euSerLysAlaLysLeuValProSerGluArgGluAlaSerProSerAsn 208

 1171 AGCTGCCAAGACTCCACGACACCGGACAACAACGAGGAGCAGCAGCCGCAG 1220
      |||||||||||||||||||||||||||||||||||||||||||||||||
  209 SerCysGlnAspSerThrAspProGluSerAsnAsnGluGluGlnArgSe 225

 1221 CGGTCTTATCTACCTGACCAACCACCATCGCCCGCACGCGCGCAACGCGTGT 1270
      |||||||||||||||||||||||||||||||||||||||||||||||||
  225 rGlyLeuIleTyrLeuThrAsnHisIleAlaArgArgAlaGlnArgValS 242
```

```
 1051 AGG...CGCTCGGAGGCACCCGCGTCCAACCACTCGGCCCAGGACAG 1097
      :::   |||||:||| |||||||||||||||||||||||
  262 LysProProSerAspGlyProArgSerAsnHisSerAlaGlnAsp.. 277

 1098 CGCCGTGGAGTACCTGCTGTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
      |||||||||||||||||||| |||||||||||||  ||| |||
  278 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 294

 1148 AGCGGAGGGCGTCCCCAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
      ||||||||||||||||||||||||||||||||||||||||||||||||
  294 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 310

 1198 AGCAACAACGAGGAGCAGCAGCCGCAGCGGTCTTATCTACCTGACCAACCACAT 1247
      |||||  |||||||||||||||||||||||||||||||||||||||||
  311 SerAsnAsnGluGluGlnGlnProGlnArgSerGlyLeuTyrLeuThrAsnHisIl 327

 1248 CGCCCGACGCGCGCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT 1294
      |  ::::|||||||||||   ||||||||||||||||||||||||
  327 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAlaT 344

 1295 ACGACCTGCTCGGCGCGCCTCCGAGAACTCGCAGGACGCGCTCCGGCGTG 1344
      ||:::||||||||||||||||||||||||::||||||||||:|||||||
  344 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 360

 1345 GTCAGCACCAGCCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCCG 1394
      |||||||||||||:|||||||||||||||||||||||||||||||||||
  361 ValSerThrSerGlyValGlnLeuLysValTyrLysCysGluHisCysAr 377

 1395 GGTGCTCTTCCTGGATCACGTCATGTACACCATCCCACATG.......G 1435
      ||||||||||||||||||||||||||||||||||||||    |
  377 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 394

 1436 GCTGCCACGGCTTCCGTGATCCTTTGAGTGCAACATGTGCGGCTACCAC 1485
      |||||||||||||||||||||||||||||||||||||||||||||||
  394 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 410

 1486 AGCCAGGACCGGTACAGAGTTCTCGTGCGCACATAAACGCGAGGGGAGCACCG 1535
      |||||||||||||||||||||||||||||||||||||||||||||||
  411 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 427

 1536 CTTCCACATGAGC 1548
      |:::||:|||
  427 gTyrHisLeuSer 431
```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-23

```
alignment_scores:
      Quality: 1740.00          Length:      376
       Ratio:  5.210             Gaps:         1
 Percent Similarity:  88.830   Percent Identity:  88.830
```

```
201 TGGGCGTGCCTGTGAAATGATGAATGGGGAAGAATGTGCGGAGGATTTACGAA 250
    |||||||||||||||||||||||||||||||||||||||||||||||||||||
53  ..................................................... 53

251 TGCTTGATGCCTCGGAGAGAAAATGAATGGCTCCCACAGGGACCAAGGC 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
53  ................................................. 53

301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGAAAACT 350
    |||||||||||||||||||||||||||||||||||||||||||||||||
53  ................................................. 53

351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGCTCATGG 400
    |||||||||||||||||||||||||||||||||||||||||||||||
53  ............................................... 53

401 TTCACAAAGAGCCACACTGGAGACGGCCCTTCCAGTGCAATCAGTGC 450
    ||||||||||||||||||||||||||||||||||
54  ...............GlyGluArgProPheGlnCysAsnGlnSer 63

451 GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
64  GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 80

501 TTCCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAACTACGCCCTGCCGCC 550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
80  sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 97

551 GGAGGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
    ||||||||||||||||||||||||||||||||||||||||
97  rgArgAspAlaLeuThrGlyHisLeuArgThrHisSer........... 109

601 CACAAATGTGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA 650
    |||||||||||||||||||||||||||||||||||||||||||||||||
109 ................................................. 109

651 GGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG 700
    |||||||||||||||||||||||||||||||||||||||||||||||||
109 ................................................. 109

701 GCACACTGTACCCAGTCATTAAAGAGAGAAACTAAGCACAGTGAAATGGCA 750
    ||||||||||||||||||||||||||||::|||:::||||||||||||||
110 .......ValIleLysGluGluThrArgAsnHisAsnGluMetAla 121

751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGTGCTGGACAGACT 800
    ||||||||||||||||:::||||||||||||||||||||||||||||
122 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 138

801 AGCAAGTAATGTCGGCCAAACGTAAGACGTCCTATGCCTCAGAAATTTCTTG 850
    ||||||||||||||||||||||||||||::|||||||:||||||
138 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 155

851 GGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAG 900
    ||||||||||||||:||||:||||||||||||||||::|||||||||||
155 lyAspLysCysLysLeuSerAspSerAspMetProTyrAspSerAlaAsnTyrGluLys 171

901 GAGAACGAAATGATGAAGTCCCACGTGACCAAGCCATCAACAACGC 950
    |||  ::||||||||||||||||||||::|||||||||||||||||
172 Glu...AspMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 187

951 CATCAACTACCTGGGGCGCCAGTCCTGCCCCGGTTGGTCAGACGCCCCC 1000
    ||||||||||||||||||||||||||||||||||||||||||||||||
187 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 204

1001 CGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAGCTGCAC 1050
     ||||::||||||||||||||  ||||||||||::||||||||||||||
204  roGlySerGluValProValIleSerSerMetTyrGlnLeuHis 220

1051 AGG...CGCTCGGAGGGCACCCCGCGCTCCAACCACTCCGCCCAGGACAG 1097
     :::  ||:::||||||||||||||||||||||||||||||||||||||
221  LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp. 236
```

```
1271 CGTCAAGGAGGAGCACCGCGGCTACGACCTGCTGCCGCCGCCCTCCGAG 1320
     |||||||||||||||||||||||||||||||||||||||||||||||||
242  erLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAlaSerGlu 258

1321 AACTCGCAGGACGCGCTCCGGTGGTCAGCACCAGCCGGGAGCAGATGAA 1370
     |||||||||||||||||||||||||||||||||||||||||||||||||
259  AsnSerGlnAspAlaLeuArgValValSerThrSerGlyGluGlnMetLy 275

1371 GGTGTACAAGTGCGAAACTGCCGGGGTGCTCTTCCTGGATCACGTCATGT 1420
     |||||||||||||||||||||||||||||||||||||||||||||||
275  sValTyrLysCysGluHisCysArgValLeuPheLeuAspHisValMetT 292

1421 ACACCATCCACATGGGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAAC 1470
     ||||||||||||||||||||||||||||||||||||||||||||||
292  yrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluCysAsn 308

1471 ATGTGCGGCTACCACAGCCAGGACCCGGTACGAGTTCTCGTCCGCCACATAAC 1520
     ||||||||||||||||||||||||||||||||||||||||||
309  MetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHisIleTh 325

1521 GCGAGGGAGCACCGCTTCCACATGAGC 1548
     ||||||||||||||||||||||
325  rArgGlyGluHisArgPheHisMetSer 334
```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622c-28

seq_documentation_block:
; Sequence 28, Application US/08733622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; CURRENT FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-733-622C-28

alignment_scores:
       Quality: 1681.00   Length: 521
        Ratio: 4.556   Gaps: 7
Percent Similarity: 70.825   Percent Identity: 65.835

alignment_block:
US-08-711-417C-165 x US-08-733-622C-28

Align seg 1/1 to: US-08-733-622C-28 from: 1 to: 390

```
1  ATGGATGCTGACGAGGGTCAAGAACATGTCTTTCTCATCAGGGAAGGAAAG 50
   |||||:::||||||||||||||||||:|||||||  |||||||||||||
1  MetAspValAspGluGlyGlnAspMetSerGlnValSerGluGlyLysGluSe 17

51 CCCCCTGTAAGCAAGATCTCCAGATGAGGGCCATGAGCCCCATGCCGATCC 100
   ||||||||||||||||||||||||||||||||||||||||:::|
17 rProProValSerAspThrProAspGluGlyAlaMetProMetProValP 34

101 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAGCAAAGCTCCAAGAGTGAC 150
   |||:|||||||||||||||||||||||||||||::|||||||
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50

151 AGAGTGCTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
   |||  |||
51 ArgGlyMet........................................ 53
```

```
1098 CGCCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
     ||||||::::  ||||||||||||||||||||||||     ||   |||
 237 .AlaValAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerG  253

1148 AGGCGGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
     ||||||||||||||||||||||||||||||||||||||||||||||
 253 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 269

1198 AGCAACAACGAGGAGGAGCGCAGCCGGTCTTATCTACCTGACCAACCACAT 1247
     |||||  |||||||||||||||||||||::||||||||||||||||
 270 SerAsnAsnGluGluGluArgSerGlyLeuIleTyrLeuThrAsnHisIl 286

1248 CGCCCGACGCGGCGCAACGC...GTGTCGTCAAGGAGGAGCACCGCGCCT 1294
     ::||||::::::  :::||||  :::||||
 286 eAsnProHisAlaArgAsnGlyLeuAlaLeuLeuSerGluGluGlnArgAlaT 303

1295 ACGAACTCGTCGCCGCCGCCTCCGAGAACTCGCAGGACACGCTCCGCGTG 1344
     ||::::||||||||||||||:::||||||
 303 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 319

1345 GTCAGACACCAGCGCGGGAGCAGATGAGGTGTACAGAGTGCCAACACTGCCG 1394
     |||||||||||::::|||||||||||
 320 ValSerThrSerGlyGlnLeuLysValTyrArgLysCysGluHisCysAr 336

1395 GGTGCTCTTCCTGGATCACGTCATGTACACCCATCCACATG.......G 1435
     |||||||||||||||||||
 336 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 353

1436 GCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCAC 1485
     ||||||||||||||
 353 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 369

1486 AGCCAGGACCGGTACGAGTTCTCGTCGCACATAAACCCGAGGGGAGCACCG 1535
     ||||||||||||||||||
 370 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGlyHisAr 386

1536 CTTCCACATGAGC 1548
     |:::|||||
 386 gTyrHisLeuSer 390
```

```
   1 ATGGATGCTGACGAGGGTCAAGACACATGTCTTCTCATCAGGAAGGAAAG  50
     |||||:::||||||||||||||||||||| |||  |||
   1 MetAspValAspGluGlnAspMetSerGlnValSerGlyLysGluSe    17

  51 CCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCC  100
     |||||||||||||||||||||||||||||||||||||||:::||
  17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP  34

 101 CCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGTCCAAGAGTGAC  150
     ||||| ||||||||||||||||||||||||::|||||||||||||||||
  34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp  50

 151 AGAGTCGTGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA  200
     ||| :::||||||||||||||||||||||||||||||||||||||
  51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs  67

 201 TGGGCGTGCCTGTGAAATGAATGGGAAGAATGTGCGAGGATTACAA     250
     ||||||||||||||:::||||||||||||||||||||||||
  67 nGlyArgAlaCysGluMetAsnGlyLysAsnValAlaGluAspLeuArgM  84

 251 TGCTTGATGCTCGGGAGAGAAATGAATGGCTCCCACAGGACCAAGGC    300
     ||||||||||||||||||||||||||||||||||||||
  84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100

 301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTGACCTTCCTAACGGAAAACT 350
     ||||||||||||||||||||||||||||||||||||
 101 SerSerAlaLeuSerGlyValGlyValGlyIleArgLeuProAsnGlyLysLe 117

 351 AAAGTGTGATATCTGTGGGATCATTGCATCGGGGCCCATGTGCTCATGG  400
     ||||||||:::|||||||||||||||||
 117 uLysCysAspIleCysGlyIleValCysIleGlyIleProAsnValLeuMetV 134

 401 TTCACAAAAGAAGCCACACTGGAGAACGGCCCCTTCCAGTGCAATCAGTGC 450
     ||||||||||||||||
 134 alHisLysArgSerHisThr............................... 140

 451 GGGGCCTCATTCACCCAGAGGGCAACCTGCTCCGGCACATCAAGCTGCA  500
     ...............................                   140

 501 TTCCGGGGAGAAGCCCTTCAAATGCCACCTCGAACTACGCCTGCCGCC   550
     ...............................                   140

 551 GGAGGGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
     ...............................                   140

 601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA 650
     ...............................                   140

 651 GGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGCCTTCCGG  700
     ...............................                   140

 701 GCACACTGTACCCAGTCATTAAAGAGAAACTAAGCACAGTGAAATGGCA  750
     ...............................                   140

 751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTGTGCTGGACAGACT  800
     ...............................                   140

 801 AGCAAGTAATGTCGCCAAACGTAAGAGTCTTATGCCTCAGAAATTTCTTG 850
     ...............................                   140

 851 GGGACAAGGGCCTGTCCGACACGCCCTACGACGTGCCACGTACGAGAAG  900
     |||||||  |||||||||||::::||||||
 141 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 157
```

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-29

seq_documentation_block:
; Sequence 29, Application US/08733622C
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287-030001
; CURRENT APPLICATION NUMBER: US/08/733,622C
; CURRENT FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/017,646
; PRIOR FILING DATE: 1996-05-14
; PRIOR APPLICATION NUMBER: US 60/005,529
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-733-622C-29

alignment_scores:
Quality: 1625.00   Length: 521
Ratio: 4.565   Gaps: 6
Percent Similarity: 68.330   Percent Identity: 63.724

alignment_block:
US-08-711-417C-165 x US-08-733-622C-29

Align seg 1/1 to: US-08-733-622C-29 from: 1 to: 376

```
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-667-2

alignment_scores:
         Quality: 1360.50       Length:   518
           Ratio:    3.436        Gaps:    11
Percent Similarity:  76.448   Percent Identity:  53.089

alignment_block:
US-08-711-417C-165 x US-10-037-667-2

Align seg 1/1  to: US-10-037-667-2  from: 1  to: 532

 76 GAGGGCGATGAGCCATGCGATCCCGAGGACCTCTCCACCACCTCGGG 125
    |||||::||:::     ::    ||   |||   ||:|||||||
 25 GluGlyGluHisAlaAsnMetAlaIleAspLeuThrSerSerThrProAs 41

126 AGGACAGCAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAATGTTAAAG 175
    :||||||||:::|||   ||:   :: ||||:|||||||:::|||||:|
 41 nGlyGlnGlnAlaSerProSerHisMetThrSerThrAsnSerValLysL 58

176 TAGAGACTCAGAGTGATGAAGAG..............AATGGGGCTGCC 210
    ::||| |||||||||||||||                    :::|||
 58 euGluMetGlnSerAspGluCysAspArgGlnProLeuSerArgGlu 74

211 TGTGAAATGAATGGGAGGAAGAATGTGCGGAGGATTACGA......ATGCT 254
    ||||||::||||:|||  :::|||:  :|||::|||       :::::|
 75 AspGluIleArgGlyHisAspGlyLySerSerLeuGluGluAlaLeuIl 91

255 TGATGCCTCGGGAGAGAGAAAATGAATGGCTCCCACAGGGACCAAGGCAGCT 304
    :::::|||          |||  ::   ||||
 91 eGluSerGluValAlaAlaAspAsnArgLysValGlnAsp.......... 104

305 CGGCTTTGCGGGAGTTGGAGGCATTGCGACTTCCTAACGGAAAACTAAAG 354
    ||:::|||    |||||||||||||||||||||||||
105 ....LeuGlnGlyGluArgGlyIleArgLeuProAsnGlyLysLeuLys 119

355 TGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGGTTCA 404
    |||||||:   |||   |:::||||||||||||||||||||||
120 CysAspValCysGlyMetValCysIleGlyProAsnValLeuMetValHi 136

405 CAAAAGAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGG 454
    |||||||||||||||::|||||||||||:::||||||||||||||||
136 sLysArgSerHisThrGlyGluArgProPheHisCysAsnGlnCysGlyA 153

455 CCTCATTCACCCAGAAGGGCAACCTCTCCCGCCACATCAAGCTGCATTCC 504
    |||||||||||||||||||||||||||||||||||::||||||||||||
153 rgSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSer 169

505 GGGGACGAAGCCCTCAAATGCCACCTCTGCAACTACGCCTGTCGCCGGAG 554
    ||||||:::|||:::||||||||||||||||||||||||:::||||||||
170 GlyGluLysProPheLysProPheCysSerProPheCysSerTyrAlaCysArgArgAr 186

555 GGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACA 604
    |||||||||||||||||||||||||||||||||||||||||||||||||
186 gAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisL 203

605 AATGTGGATATTGTGCCGAAGCTATAAACAGGCATATAAACGTCTTTAGGAGAA 654
    ||:::|||:::||||||||||||||||||||||
203 ysCysAsnTyrCysGlyArgSerTyrLysGlnArgThrSerLeuGluGlu 219

655 CATAAAGAGCCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCAC 704
    ||||||||||||||||||||||||||||||||||||||||
219 HisLysGluArgCysHisAsnTyrLeuGlnIleAsnValSerMetGluAlaAl 236

705 A...........CTGTACCCAGTCATTAAAGAAGAAAACTA 733
    :::         |||::::     ||  ||:::|||
236 aGlyGlnValMetSerHisHisValProProMet.....GluAspCysL 251

734 AGCACAGTGAA.....ATGGCAGAAGACCTGTGCAAGATAGATCAGAG 777
    ||:::::||||                  |||
251


901 GAGAACGAAATGATGAAGTCCACGTGATGGACCAAGCCATCAACAACGC 950
    |||  ::|||||     ||||||||||||||||||||||||||
158 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 173

951 CATCAACTACCTGGGGGCCCAGTCCCTGCGCCCCTGGTGCAGACGCCCC 1000
    |||||||||||||||||||||||||||||||||||||||||||||||
173 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 190

1001 CGGGCGGTTCCGAGTGGTCCGGTCATCAGCCCGATGGTACCAGCTGCAC 1050
     ||||:::||||||||||||||||||||||||||||||||||||||||
 190 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 206

1051 AGG...CGGTCGGAGGGCACCCCGCCGCCTCCAACCACTCGGCCCAGGACAG 1097
      :::   ||:::||  |||||||||||||||||||||||||
 207 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 222

1098 CGCCTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
     |||:||||  |||||||||||||||||| || |||||||
 223 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 239

1148 AGCGCGAGGGGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
     |||||||||||||||||||||||||||||||||:||||||||||||||
 239 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 255

1198 AGCAACAACGAGGAGCAGCGCAGCGGTCTTATCTACCTGACCAACCACAT 1247
     |||||||||||||||||||||||||||||||||||||||||||||
 256 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIl 272

1248 CGCCCGACCGCCGCAACGC...GTGTCGCTCAAGGAGGAGCACCGCGCCT 1294
      :::||||       ||||   |||:::|||||||||||||||||||||
 272 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnLeuGlnArgAlaT 289

1295 ACGACCTGCTGCGCGCCCTCCGAGAACTCGCGAGGACGCGCTCCGCGTG 1344
     |:::::||||||||||||||||||||:::|||||
 289 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAsnSerAlaPheArgVal 305

1345 GTCAGCACCAGCCGGGGAGCCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394
     ||:::|||||||||||||||||||||||||||||||||||||:||||||
 306 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 322

1395 GGTGCTCTTCCTCGGATCACGTCATGTACCACCATCCCACATG.......G 1435
     |:::::||||||||||||||||||||||||::|:::|||||
 322 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 339

1436 GCTGCCACGGCGGCTTCCGTGATCCTTTGAGTGCAACATGTGCGGCTACCAC 1485
     |||||||||||||||||||||||||||||||||||||||||||||||
 339 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 355

1486 AGCCAGGACCGGTACGAGTTCTCGTCCGCCACATAACGCGAGGGGAGCACCG 1535
     |||||||||||||||||||||||||||||||||||||||||||||
 356 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyHisGluHisAr 372

1536 CTTCCACATGAGC 1548
     :::||::|||
 372 gTyrHisLeuSer 376
```

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-2

; Sequence 2, Application US/0873362ZC
; GENERAL INFORMATION:
;   APPLICANT: Georgopoulos, Katia
;   APPLICANT: Morgan, Bruce A.
;   TITLE OF INVENTION: AIOLOS GENE
;   FILE REFERENCE: 10287-030001
;   CURRENT APPLICATION NUMBER: US/08/733,622C
;   CURRENT FILING DATE: 1996-10-17
;   PRIOR APPLICATION NUMBER: US 60/017,646
;   PRIOR FILING DATE: 1996-05-14
;   PRIOR APPLICATION NUMBER: US 60/005,529
;   PRIOR FILING DATE: 1995-10-18
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-08-733-622C-2

alignment_scores:
               Quality: 1302.00   Length: 526
                 Ratio: 3.305   Gaps: 16
  Percent Similarity: 74.905   Percent Identity: 52.281

alignment_block:
US-08-711-417C-165 x US-08-733-622C-2   .

Align seg 1/1 to: US-08-733-622C-2   from: 1   to: 507

   25 ATGTCTTTCTCATCAGGGAAGGAAGAAAGCCCCCTGTAAGCGATACTCCAGA 74
      ||| ::||||| :::||||||::||||::|||::||||
    8 ValGluLeuLysSerThrGluGlnProLeuProThrGluSerProAsn   24

   75 TGAG...GGCGATGAGCCCATGCCATCCCGAGGACCTCTCCACCACCT 121
      ::||| ||| |||:::::||||||:::::||||||||||||
   24 pAlaLeuAsnAspTyrSerLeuProLysProHisGluIleGluAsnValA 41

  122 CGGGAGGGACAGCAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAAT... 168
      ::::: ::: |||||:::||||||:::||| : :|||||||:::
   41 spSerArgGluAlaProAlaAsnGluAspGluAspAlaGlyGluAspSer 57

  169 ......GTTAAAGTAGAGACTCAGAGTGATGAAGAGAATGGGCGTGCCTG 212
      :   ::|||||::::: ::: :::||||||
   58 MetLysValLysAspGluTyrSerAspArgAspGluAsnIleMetLysPr 74

  213 TGAAATGAATGGGAAGAAATGTGCGGAGGATTTACGAATGCTTGATGCCT 262
      || :::||| ||||||||||||||::::::
   74 oGluProMetGly.................................AspAlaG 81

  263 CGGGAGAGAAAATGAATGCTCCCACAGGGACCAAGGCAGCTCGGCTTTG 312
      ::::: :::: |:::|||||||||:::||| :|||::|||
   81 luGluSerGluMetProTyrSerThrAlaArgGluTyrSerAspTyrGlu 97

  313 TCG.............................GGAGTTGGAGGCATTCGACTTCCTAA 341
      ||| :: ||||||||||
   98 SerIleLysLeuGluArgHisValProTyrAspAsnSerArgProThrSe 114

  342 CGGAAAACTAAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATG 391
      :|||||::|||:|||||| :::|||||:::|||||:::||||||||
  114 rGlyLysMetAsnCysAspValCysGlyLeuSerCysIleSerPheAsnV 131

  392 TGCTCATGGTTCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGC 441
      ||||||||||:::::::|||||||||||:::||||||||||||||||||
  131 alLeuMetValHisLysArgSerHisThrGlyGluArgProPheGlnCys 147

  442 AATCAGTGCGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGACACAT 491
      :|||||||||||||||:::||||||:::|||||||||::||||||||||
  148 AsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIl 164

  492 CAAGCTGCATTCCGGGAGAAGCCCTTCAAATGCCACCTCTGCAACTACG 541
      |||||||||||:::::::||||||||||||||||||||||||||||||
  251 ysGluGlnProIleMetAspAsnAsnIleSerLeuValAlaPheGlu 267

  778 AGATCTCTGTGCTGGACAGACTAGCAAGTAATGTCGCCAAACGTAAGAG 827
      |||:::::::||::::|:::||||||||||||||||||||||||||
  268 ArgProAlaValIleGluLysThrLeuAlaAsnMetGlyLysArgLysSe 284

  828 CTCTATGCCTCAGAAATTTCTTGGGACAAGGGCCTGTCCGACACGCCCT 877
      ||| |||:::|| :::   :::
  284 rSerThrProGlnLysPheValGlyGluLysLeuMetArgPheSerTyrP 301

  878 ACGAC............AGTGCCACGTACGAGAGGAGAACGAAATG 912
      |||| ::: |||||||||||||| |||:::
  301 roAspIleHisPheHisMetAsnLeuThrTyrGluLysGluAlaGluLeu 317

  913 ATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAACTACCT 962
      |||:::::||||::::::|||||||||||||||||||||:::||:||||
  318 MetGlnSerHisMetMetAspGlnAlaIleAsnAsnAlaIleThrTyrLe 334

  963 GGGGGCCGAGTCCTGCGCCCCGTGGTCAGACGCCCCCGGCCGGT...T 1009
      |||:::||||||:::||::::::|||||||::::::|:::||::
  334 uGlyAlaGluAlaLeuHisProLeuMetGlnHisAlaProSerThrIleA 351

 1010 CCGAGGTGGTCCCGGTCATC............AGCCCGATGTACCAGCTG 1047
      ::|||||||::|||||||| ||| :::||||||:::
  351 laGluValAlaProValIleSerSerAlaTyrSerGlnValTyrHisPro 367

 1048 CACAGGCGGCTCGGAGGGCACCCCGGCTCCAAACACTCGGCCCAGGACAG 1097
      |||:::|| ::::: |||||||:::||||||||::::||||||
  368 AsnArgIleGluArgProIleSerArgGluThrSerAspSerHisGluAs 384

 1098 CGCCGTGGAGTACCTGCTGTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
      : ||||||||||||||::::|||||||||:::||||||||||||
  384 nAsnMetAspGlyProIleSerLeuIleArgProLysSerArgProGlnG 401

 1148 AGCGCGAGGGCGTCCCGAGCAACAGTCCCACGGACACCGAG 1197
      |||||||||||||||||||||||||:::|||||||||:::|||
  401 luArgGluAlaSerProSerAsnSerCysLeuAspSerThrAspSerGlu 417

 1198 AGCAACAACGAGGAGCAGCCAGCGGTCTTATCTACCTGACCAAC..... 1242
      |||:::::::||||||||| :::||| |||
  418 SerSerHisAspAspArgGlnSer........TyrTyrGlnGlyAsnProAl 431

 1243 ...CACATCGCCCGACGGCGCAACGCGTCGCTCAAGGAGGAGCACC 1288
      ::: ||| || :::|||||||||||||::||:::
  431 aLeuAsnProLysArgLysGlnSerProAlaTyrMetLysGluAspValL 448

 1289 GCGCCTACGACCTGCTGCGGCGCCTCCGAGAACTCGCAGGACGCGCTC 1338
      |||:::||| ||| :::   :::||||||||||||||||
  448 ysAlaLeuAspAlaThrLysAlaProLysGlySerLeuLysSerAspIleTyr 464

 1339 CGCGTGGTCAGCACCAGCGGGAGCCAGATGAAGGTGTACAAGTGCGAACA 1388
      :::|| |||:::   :::|||||||| |||||||
  465 LysValPheAsnGlyGluGlyGluGlnIleIleArgGluAlaPheLysCysGluHi 481

 1389 CTGCCGGGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATGGGCT 1438
      |||||||||||||||||:::::::||||||||||||||||||||||||
  481 sCysArgValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyC 498

 1439 GCCACGGCTTCCGTGATCCTTTGAGTGCAACATGTGCGGCTACCACAGC 1488
      |:::::::::||||||||||::: :::|||||:||||||||||||||
  498 YSHisGlyThrArgAspProLeuGluCysAsnIleCysGlyTyrArgSer 514

 1489 CAGGACCGGTACGAGTTCTTCGTGCACATAACCGAGGGAGCCACCGCTT 1538
      ||||||::||:::||||||||:::||| :::||||||||||:::||
  515 GlnAspArgTyrGluPheSerGlyHisSerHisIleValGlyGlyGlnHisThrPh 531

 1539 CCAC 1542
      ||||
  531 eHis 532

seq_name: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:US-08-733-622C-2

seq_documentation_block:

```
164 eLysLeuHisThrGlyGluLysProPheLysCysHisLeuCysAsnTyrA 181
542 CCTGCCGCCGGAGGACGGCCCTCACTGGCCACCTGAGGACGGCACTCCGTT 591
    ||||:::||||||||||||||||||||||||||||||
181 laCysGlnArgArgAspAlaLeuThrGlyHisLeuArgThrHisSerVal 197
592 GGTAAACCTCACAAATGTGGATAATGTGCGGCTACTATAAACAGCGAAC 641
    ::||||||||||||||||||||||||||||||:::
198 GluLysProTyrLysCysGlyPheCysGlyArgSerTyrLysGlnArgSe 214
642 GTCTTTAGAGAACATAAAGAGCGCTCCCACAACTACTTGGAAAGCATGG 691
    :||||||||||||||||||:::||:||||:::
214 rSerLeuGluHisLysGluArgCysArgAlaPheLeuGlnAsnProA 231
692 GCCTTCCGGCACACTGTACCCAGTCATTAAAGAAGAAAACTAAGCACAGT 741
    ||||:::||:::||
231 spLeu...GlyAspAlaAlaSerVal.......GluAlaArgHisIle 243
742 GAAATGGCAGAGACCTGCAAGATAGGATCAGAGAGATCTCTCGTGCT 791
    ::||||||||||:::||||||
244 Lys..............AlaGluMetGlySerGluArgAlaLeuValLe 255
792 GGACAGACTAGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGA 841
    ||||||||||||||||||||||||||||||||
255 uAspArgLeuAlaSerAsnValAlaLysArgLysSerSerMetProGlnL 272
842 AATTTCTTGGGGACAAG...GGCCGTCCGACACGCCCTACGACAGTGCC 888
    ::|||||:::|||:::||:::
272 ysPheIleGlyGluLysArgHisCysPheAspAlaAsnTyrAsnProGly 288
889 ..ACGTACGAGAAGGAGAACGAAATGATGAAGTCCCACGTGATGGACCA 935
    ||||||||||:::|||||||:::|||||||
289 TyrMetTyrGluLysGluMetMetGlnThrArgMetMetAspGl 305
936 AGCCATCAACAACGCCATCAACTACCTGGGGCCGAGTCCCTGCGCCCGC 985
    |||||||||||||||||||
305 nAlaIleAsnAsnAlaIleLeuSerTyrLeuGlyAlaGluAlaPheArgProL 322
986 TGGTGCAGACGCCCCGGGGC...GGTTCCGAGGTGGTCCCGGTCATCAGC 1032
    |||||||||||:::||||||
322 euValGlnThrProProAlaProThrSerGluMetValProValIleSer 338
1033 CCGATGTACCAGCTGCAC..AGGCCGTCGGAG........GGCACCCC 1070
     ::|||:::||||||
339 SerValTyrProIleAlaLeuThrArgAlaAspMetProMetGlyAlaPr 355
1071 GCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGAGTACCTGCTGCTGC 1120
     |:::|||||||||||||||||||||||||
355 oGlnGlu...............MetGluLysLysArgIleL 364
1121 TCTCCAAGGCCAAGTGGTGCCCTCGGAGCGCGGAGGGTCCCCGAGCAAC 1170
     ||||||||||||:::|||
364 euLeuProGluLysIleLeuProSerGluArgGlyLeuSerProAsnAsn 380
1171 AGCTGCCAAGACTCCACGGACACCGAGAGCGACAACGAGGAGCAGCCGCAG 1220
     :::||||||||||||||||||||
381 SerAlaGlnAspSerThrAspThrGluSerAsnHisGluAspArgGlnHi 397
1221 CGGTCTTATCTACCTGACCAACCACATC...........GCCCGACCGCG 1258
     :::||||:::||||
397 s......LeuTyrGlnGlnSerHisValLeuProGlnAlaArgAsnG 412
1259 CGCAACGCCGTGTGCGTCAAGGAGGAGCACCGCGCTACGACCTGCTGCGCC 1308
     :::|||:::|||||||||||
412 lyMetProLeu...LeuLysGluValProArgSerPheLeuLeuLys 427
1309 GCCGGCCTCCGAGAACTCGCAGGACGCGCGCTCCGCGTGGTCAGCACCAGCGCGG 1358
     :::||:::||||||
428 ProProProIleCysLeuArgAspSerIleLysValIleAsnLysGluGl 444
1359 GGAGCAGATGAAGTGTACAAGTCGCAACTGCCGGGGTGCTCTTCCTCG 1408
     ||||||||||||||||||||||
444 yGluValMetAspValPheArgCysAspHisCysHisValLeuPheLeuA 461
```

```
1409 ATCACGTCATGTACCACCATCCACATGGCTGCCACGGCTTCCGTGATCCT 1458
     ::||||:::||||||||||||||||||||||||||||||
461 spTyrValMetPheThrIleHisMetGlyCysHisSerGlyPheArgAspPro 477
1459 TTTGAGTGCAACATGTGCGGCTACCACCAGGACCGGTACGAGTTCTC 1508
     |||||||||||||||:::|||||||||::||||
478 PheGluCysAsnMetCysGlyTyrArgSerHisAspArgTyrGluPheSe 494
1509 GTCGCACATAACGCGAGGGAGGCACCGC 1536
     ||||||:::||||||||||||
494 rSerHisIleAlaArgGlyGluHisArg 503
```

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-3

```
alignment_scores:
        Quality:  1301.00                        Length:  526
        Ratio:       3.310                        Gaps:     16
        Percent Similarity: 74.715    Percent Identity: 52.281

alignment_block:
US-08-711-417C-165 x US-10-037-667-3  ..

Align seg 1/1  to: US-10-037-667-3  from: 1  to: 507

25 ARGTCTTTCTCATCAGGGAGGAAGGAAAGCCCCCTGTAAGCGGGATACTCCAGA 74
   ::|||||||||||||:::||:::||:::|:::||||
8 ValGlyLeuLysSerThrGlyGluGlnProLeuProThrGluSerProAs 24
75 TGAG...GGCGATGAGCCCATGCGATCCCCGAGGACCTCTCCACCACCT 121
   :::|||  |||:::||||||||
24 pAlaLeuAsnAspTyrSerLeuProLysProHisGluIleGluAsnValA 41
122 CGGGAGGACAGCAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAAT... 168
   :::|||   :::||||||||||||||:::|||
41 spSerArgGluAlaProAlaAsnGluAspGluAspAlaGlyGluAspSer 57
169 ......GTTAAAGTAGAGACTCAGAGTGATGAAGAAGAGATGGGGTGCCTG 212
   :::|||||||||||||||||||:::
58 MetLysValLysAspGluTyrSerAspArgAspGluAsnIleMetLysPr 74
213 TGAAATGAATGGGGAAGAATGTCGCGGAGGATTTACGAATGCTTGATGCCT 262
   :::|||||||||||||||||||||
74 oGluProMetGly.............................AspAlaG 81
263 CGGGAGAGAAAATGAATGGCTCCCACAGGGACCAAGCCAGCTCGGCTTTG 312
   |||:::|||
81 luGluSerGluMetProTyrSerPheTyrAlaArgGluTyrSerAspTyrGlu 97
313 TCG.................................GGAGTTGGAGGCATTCGACTTCCTAA 341
   |||  :::
98 SerIleLysLeuGluArgHisValProTyrAspAsnSerArgProThrSe 114
```

```
342 CGGAAAACTAAAGTGTGATATCTCTGGGATCATTGCATCGGCCCCAATG 391
    :||||||::::  ||||||:  ||||||::  |||
114 rGlyLysMetCysAspValCysGlyLeuSerCysPheAsnV 131

392 TGCTCATGGTTCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGC 441
    ||||||||||||||||||||||||||||||||||||||||||||
131 aILeuMetValHisLysArgSerHisThrGlyGluArgProPheGlnCys 147

442 AATCAGTGCGGGGCCTCATTCACCCAGAAGGCAACCTGTCTCCGGCACAT 491
    |||||||||||||||||  :||||||||||||||||||||||
148 AsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIl 164

492 CAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCCTCTGCAACTACG 541
    |||||||||:::||||||||||||||||||||||||||||
164 eLysLeuHisThrGlyGluLysProPheLysCysHisProLeuGlnTyrA 181

542 CCTGCCGCCGAGGGACGGCCCTCACTGGCCACCTCGAGGACGCACTCCGTT 591
    |||||||||:::||||||||||||||||||||||||||
181 laCysGlnArgArgAspAlaLeuThrGlyHisLeuArgThrHisSerVal 197

592 GGTAAACCTCACAAATGTGGATAATTGTGCCGAGCTATAAACAGCGAAC 641
    ||||||:::||||   ::||||||||||||||||||||
198 GluLysProTyrLysCysGlyPheCysGlyArgSerTyrLysGlnArgSe 214

642 GTCTTTAGAGGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGG 691
    :||||||||||||||||||||:  ::|||:::::::
214 rSerLeuGluHisLysLysGluArgCysAsnTyrLeuGluSerMetGly 231

692 GCCTTCCGGCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGT 741
    |||  |||      |||          :::|||
231 spLeu...GlyAspAlaAlaSerVal.......GluAlaArgHisIle 243

742 GAAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGATCTTCGTGCT 791
    :::            :::||||||||||||||||||||||
244 Lys.........AlaGluMetGlySerGluArgAlaLeuValLe 255

792 GGACAGACTAGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGA 841
    |||||||||||||||||||||||||||||||||
255 uAspArgLeuAlaSerAsnValAlaLysArgLysSerSerMetProGlnL 272

842 AATTTCTTGGGGACAAG...GGCCGTGTCCGACACGGCCCTACGACAGTGCC 888
    ||||||            :::    ::::
272 ysPheIleGlyGluLysArgHisCysPheAspAlaAsnTyrAsnProGly 288

889 ...AGTACGAGAAGAAGGAACGAAAATGATGAAGTCCCACGTGATGGACCA 935
    ||||||||||||||||||||||:::::::::||||||
289 TyrMetTyrGluLysGluMetMetGlnThrArgMetMetAspGl 305

936 AGCCATCAACACGCCATCAACTACCTGGGGCCGAGTCCCTGCCCCGC 985
    ||||||||||||||||||||||||||:::||||||
305 nAlaIleAsnAsnAlaIleSerTyrLeuGlyAlaGluAlaPheArgProL 322

986 TGGTGCAGAGCCCCCCGGGC...GGTTCCGAGGTGGTCCCGGTCATCAGC 1032
    |||:||            ||||||||||||||||:||||||
322 euValGlnThrProAlaProThrSerGlnMetValProValIleSer 338

1033 CCGATGTACCAGCTGCAC...AGGCGCTCGGAG........GGCACCCC 1070
     :::|||     :::      |||:::||
339 SerValTyrProIleAlaLeuThrArgAlaAspMetProMetGlyAlaPr 355

1071 GCGCTCCAACCACTCGGCCCCAGGAGACGCCGGCCGGTGGAGTACCTGCTGC 1120
     |::::::                   :::|||
355 oGlnGlu.......................MetGluLysLysArgIleL 364

1121 TCTCCAAGGCCAAGTTGGTGCCCCTCGGAGCGCAGGCGCTCCCCGAGCAAC 1170
     ||.          ||||||||||||||||||||
364 euLeuProGluLysIleLeuProSerGluArgGlyLeuSerProAsnAsn 380

1171 AGTTGCCAAGACTTCCACGGACACCGAGCGACCAACAAGCAGGAGCAGCCCAG 1220
     ||||||||||||||::::||||||::||||||||||
381 SerAlaGlnAspSerThrAspThrSerAsnHisGluAspArgGlnHi 397

1221 CGGTCTTATCTACCTGACCACCACATC........GCCCGACGCGG 1258
     ||||||||||||||               :::||||||
```

```
397 s......LeuTyrGlnGlnSerHisValLeuProGlnAlaArgAsnG 412
    :::|||                ||||||:::::

1259 CGCAACGCCGTGCTGCTCAAGGAGGAGCACCGGCCGCCTACGACCTGCTGCGC 1308
     :::: :: :|||||||       |||||||::::|::||:
412 lyMetProLeu...LeuLysGluValProArgSerPheGluLeuLeuLys 427

1309 GCCGGCCTCCGAGAACTGCGAGACGCGGCTCCCGCTGGTCAGCACCAGCGG 1358
     |||||||||||||||||||:::||::||||:  :::||
428 ProProProIleCysLeuArgAspSerIleLysValIleAsnLysGluGl 444

1359 GGAGCAGATGAAGGTGTACAAGTGCAACACTGCCGGTGCTCTTCCTGG 1408
     ||||   ||| |||:::::||||||:::::|||||||||||||||||
444 yGluValMetAspValPheArgCysAspHisCysHisValLeuPheLeuA 461

1409 ATCACGTCATGTACACCATCCACATGGCTGCCACGCTTCCGTGATCCT 1458
     ||:::|||||:::||||||||||||||||||||||||||||||||||||
461 spTyrValMetPheThrIleHisMetGlyCysHisGlyPheArgAspPro 477

1459 TTTGAGTGCAACATGTGCGGCTACCACAGCCAGGACCGGTACGAGTTCTC 1508
     ||||||||||||||||||||||||:::||||||||||||||||||||||
478 PheGluCysAsnMetCysGlyTyrArgSerHisAspArgTyrGluPheSe 494

1509 GTCGCACATAACGCGAGGGAGCACCGC 1536
     ||||||||||||||||||||||||||
494 rSerHisIleAlaArgGlyGluHisArg 503
```

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-1

alignment_scores:
```
           Quality: 1282.50          Length:       532
             Ratio:   3.402            Gaps:        16
Percent Similarity:  70.865   Percent Identity:  50.752
```

alignment_block:
US-08-711-417C-165 x US-10-037-667-1

Align seg 1/1 to: US-10-037-667-1 from: 1 to: 537

```
US-10-037-667-1 from: 1 to: 537

94 CCGATCCCGAGGACCTCTCCACCACCTCGGAGGACGCAAAGCTCCAA 143
   |||::            :::|||||||:::  |||||||||
22 ProValGlyProSerValSerThrProAsn...SerGlnHisSerSerPr 37

144 GAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATG 193
   |||  :::  |||||||||||||||:::||||||||||||||||
37 oSerArgSerLeuSerAlaAsnSerIleLysValGluMetTyrSerAspG 54

194 AAGAGAAATGGGCGTGCCTCTGAAATGAATGAATGGGAAGAAGAATGTCCGGAGGAT 243
   ||||||:::|||                   :::    |||
54 luGluSerSerArgLeu.......................LeuGlyProAsp 63

244 TTACGAATGCTTGATGCCTCGGCGAGAGAAAATG..................... 276
   ||||:||||||                        :::  :::
```

```
  64 GluArgLeuLeuAspLysAspSerValIleValGluAspSerLeuSe  80
 277 ......................AATGGCTCCCACAGGAGCACCAAGGCAGCTCGG 307
  80 rGluProLeuGlyTyrCysAspGlySerGlyProGluProHisSerPro.  96
 308 CTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACTAAAGTGT 357
  97 .............GlyGlyIleArgLeuProAsnGlyLysLeuLysCys  108
 358 GATATCTGTGGGATCATTTGCATCGGGCCCAATGCTCATGGTTCACAA  407
 109 AspValCysGlyMetValCysIleGlyProAsnValLeuMetValHisLy  125
 408 AAGAAGCCACACTGGAGACGGCCCTTCCAGTGCAATCAGTCGCGGGGCCT  457
 125 sArgSerHisThrGlyGluArgProPheHisCysAsnGlnSerCysGlyAlaS  142
 458 CATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGG  507
 142 erPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGly  158
 508 GAGAAGCCCTTCAAATGCCACCCTCGCAACTACGCCTGCCCGCCGAGGGA  557
 159 GluLysProPheLysCysProPheCysAsnTyrAlaCysArgArgArgAs  175
 558 CGCCCTCACTGCCCACCTGAGGAGGCACTCC..............GTTG  592
 175 pAlaLeuThrGlyHisHisLeuArgThrHisSerValSerSerProThrValG  192
 593 GTAAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACG  642
 192 lyLysProTyrLysCysValSerAsnTyrCysSerGlyArgSerTyrLysGlnSer  208
 643 TCTTTAGAGGAACATAAAGAGCGCTGCCACAACTACTTGAAAAGCCATG.  690
 209 ThrLeuGluGluHisLysGluArgCysHisAsnTyrLeuGlnSerLeuSe  225
 691 .......................GGCCTTCCGGGCACACTGTACCCAGTCA  718
 225 rThrAspAlaGlnAlaLeuThrHrGlyGlnProGly...............  236
 719 TTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGAC...CTGTGCAAG  765
 237 .....AspGluIleArgAspLeuGluMetValProAspSerMetLeuHis  251
 766 ATAGGATCAGAGAGATCTCGTGCTGACAGACTAGCCAAGTAATGTCGC  815
 252 ProSerThrGluArgProThrPheIleAspPArgLeuAlaAsnSerLeuTh  268
 816 CAAAGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAG..........  858
 268 rLysArgLysArgSerThrProGlnLysPheValGlyGluLysGlnMetA  285
 859 .....GGCCTGTCCGACACCCCCTACGAC.......AGTCCCACGTAC  894
 285 rgPheSerLeuSerAspLeuProTyrAspValAsnAlaSerGlyGlyTyr  301
 895 GAGAAGGAGAACGAAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAA  944
 302 GluLysAspValGluLeuValAlaAlaHisHisGlyLeuGluProGlyPheGl  318
 945 CAACGCCATCAACTACCTGGGGCCCAGTCCCTGCGCCCCTGGTCGCAGA  994
 318 yGlySerLeuAlaPheValGlyThrGluHisLeuArgProLeu...ArgL  334
 995 CGCCCCCGGGCCGT..........TCCGAGGTGGTCCCGTCATCAGCCCGATG 1038
 334 euProProThrAsnCysIleSerGluIleThrProValIleSerSerVal  350
1039 TAC.................CAGCTCCACAGGCGCCTCGGAG......GGCACCCC 1070
 351 TyrThrGlnMetGlnProIleProSerArgLeuGluLeuProGlySerAr  367
```

```
1071 GGCCTCCAACCACTCGGCCCAGGACAGCGCCGTGGAGTACCTGCTGCTGC 1120
 367 gGluAlaGlyGluGlyProGluAspLeuGly...AspGlyGlyProLeuL  383
1121 TCTCCAAGGCCAAGTTGGTGCCCTCGGAGCGGAGGCGTCCCGAGCAAC 1170
 383 euTyrArgAlaArgGlySerLeuThrAspProGlyAlaSerProSerAsn  399
1171 AGTGCCAAGACTCCACGGACACCGAGGAGCAACCAGGAGCAGCGCAG 1220
 400 GlyCysGlnAspSerThrAspThrGluSerAsnHisGluAspArgIleGl  416
1221 CGGTCTTATCTACCTG.............................ACCA 1240
 416 yGlyValValSerLeuProGlnGlyProProProGlnProProProThrI  433
1241 ACCACATGCCCCGACGCGCGCAACGCGTGTCGCTCAAGGAGGAGCACCGC 1290
 433 leValValGlyArgHisSerProAlaTyrAlaLysGluAspProLysPro  449
1291 GCCTACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCAGGACGGCGCTCCG 1340
 450 GlnGluGlyLeuLeuArgGlyThrProGlySerLysGluValLeuAr  466
1341 CGTGGTCAGCACCACGCGGGAGCAGATGAAGGTGTACAGTGCGAACACT 1390
 466 gValValGlyGluSerGlyGluProValLysAlaPheLysCysGluHisC  483
1391 GCCGGGTGCTCTTCCTGGATCACGTCATGTACACCATCCACATGGGCTGC 1440
 483 ysArgIleLeuPheLeuAspHisValMetPheThrIleHisMetGlyCys  499
1441 CACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCA 1490
 500 HisGlyPheArgAspProPheGluCysAsnIleCysGlyTyrHisSerGl  516
1491 GGACCGGTACGAGTTCTGTCGCCACATAACGCGAGGGAGCACCGC 1536
 516 nAspArgTyrGluPheSerHisIleValArgGlyHisLys 531
```

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-037-667-5

```
alignment_scores:
     Quality:  1126.00                Length:  546
       Ratio:     3.283                 Gaps:   17
Percent Similarity:  62.821   Percent Identity:  44.322

alignment_block:
US-08-711-417C-165 x US-10-037-667-5   ..
US-10-037-667-5   from: 1   to: 498

Align seg 1/1   to: 1   to: 498
```

Wed Aug 28 10:05:41 2002

us-08-711-417c-165.rapn

```
  64 GATACTCCAGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTC 113
     |||  |||            |||||::          :: :: |||||::||
  27 AspArgProLysAlaGlyAspSer......SerLeuGluLysAspPheSe 41

 114 C............................ACCACCTGGGAGGACAGCAAAGCT 139
                                   |||::||          :::|||   |||
  41 rAspAlaLeuIleGlyProThrValSerThrProAsnSerArgHisSerS 58

 140 CCAAGAGTGACAGACTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGT 189
     ||  |||          |||||||:::|||||||||  |
  58 erProSerArgSerArgSerAlaAsnSerIleLysValGluMetTyrGly 74

 190 GATGAAGAGAATGGGCGCGTGCCTGTGAA.................... 216
     |||::||||                :||||
  75 AspAspGluSerGlyArgLeuLeuSerHisGluSerGlyLeuGluLy 91

 217 ........ATGAATGGGGAAGAAATGTGCGGAGGATTTACGAAATGC 253
               ||||||          :::|||  |||
  91 sGluAspGluIleMetGlyAspAspSerLeuValGluProLeuGlyTyrC 108

 254 TTGATGCCTCGGGAGAGAAAATGAATGGCTCCCACAGGACCAAGGCAGC 303
     |||          :::|||          |||::::
 108 ysAspGlyProGlyGlnAspProHisSerPro............... 118

 304 TCGGCTTTGTCGGAGTTGGAGGCATTCGACTTCCTAACGGAAAAACTAAA 353
                                       |||||| ||||||||||||||
 119 ...............GlyIleLeuLeuProAsnGlyLysLysLeuLy 128

 354 GTGTGATATCTGTGGGATCATTTGCATGCGGGCCCAATGTGCTCATGGTTC 403
     ||||||||||::|||||||||::||||||||||||||||||||
 128 sCysAspIleCysGlyMetValCysIleGlyProAsnValLeuMetValH 145

 404 ACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGG 453
     |||||||||::|||||||||  :||||||||||||||||||||
 145 isLysArgSerHisThrGlyGluArgProPheHisCysAsnGlnCysGly 161

 454 GCCTCATTCACCCAGAGAGGGCAACCTGCTCCGGCACATCAAGCTGCATTC 503
     |||  ||||||||||||||||||||::||||||||||||||||||||
 162 AlaProPheThrGlnLysLysAsnLeuLeuArgHisIleLysLeuHisSe 178

 504 CGGGGAGAAGCCCTTCAAATGCCACCTCTGCAACTACGCCTGCCGCCCGA 553
     ||||||||||::||||||||||||||||||||||||||||||||
 178 rGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgA 195

 554 GGACGCGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCAC 603
     ||||||||||::||||||||||||||||::||||||||||||||||
 195 rgAspAlaLeuSerGlyHisLeuArgThrHisAlaValGlyLysProTyr 211

 604 AAATGTGATATTGTGCCGAAGCTATAAACAGCGAAACGTCTTTAGAGGA 653
     ||||||||||||||||::||||||||||::||||::||||||
 212 LysCysAsnTyrCysGlyLysArgSerTyrLysGlnAsnThrLeuGluGl 228

 654 ACATAAAGAGGCTGCCACAACTACTTGGAAAGCATGGCCTTCCGGGCA 703
     ||||||||||||::||||||||||::|||||||||||||||||
 228 uHisLysGluArgCysHisAsnTyrLeuGlnSerLeu.......... 240

 704 CACTGTACCCAGTCATTAAAGAAGAAAACTAAGCACAGTGAAATGGCAGAA 753
                                       ||
 240 ................................................ 240

 754 GACCTGTGCAAGATAGGATCAGAGATCTCTGCTGCTGGACAGACTAGC 803
 240 ................................................ 240

 804 AAGTAATGTCGCCAAACGTAAGACTCTATGCCTCAGAAATTTCTTGGGG 853
     ||||||::||:::     :: |||   |||::::::
 241 .SerAsnGluAlaGlnHisLeuProAlaHisProGlyGluTrp...GlyP 256

 854 ACAAGGGC................................ 861
     ::|||
 256 roGlnGlyLysAsnCysIleCysThrArgGluLysGlnMetArgLeuSer 272

 862 CTGTCCGACACGCCCTACGAC...AGTGCCACGTACGAGAGGAGAACGA 908
```

```
     |||::|||  ||||||||
 273 LeuAlaAspLeuProTyrGlnMetSerSerPheGluLysAspValGl 289

 909 AATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAACT 958
     |||||||||          :: ||| |||::|||     ::|||:::::
 289 uIleValSerHisHisProLeuAspThrAlaTyrGlyAsnSerLeuAlaP 306

 959 ACCTGGGGCCGGAGTCCGTGCGCCCCGTCGTGAGACGCCCCGGGCGGT 1008
     ::::||||||                |||||          ||||||  |||
 306 heValGlyGlyPro...........MetArgLeuProProThrAsn 317

1009 ......TCCGAGTGGTCCGGTCATCAGCCCATGTACCAGCTGCACAG 1052
           ||||||::::||||||||||||  :::||
 318 CysIleSerGluIleThrProValIleSerServalTyrThrGlnLeuGl 334

1053 GCGCTCGGAGGGCACCCCG......CGCTCCAACCACTCGGCCCCAGGACA 1096
     :   |||||||||||     :::||| |||   :::
 334 nProMetGlnGlyArgProAspMetProGlyAsnArgGluAlaAlaGluG 351

1097 GCGCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCC.... 1143
     ::  :::                |||          :::||
 351 lyHisGluAsp............................IleProAsp 357

1144 ....................TCGGAGGCGGAGGCGTCCCCGAG 1166
                          ||||||||    ||||||||||
 358 GlyThrGlnIleHisTyrArgGlyArgSerGluHisGlyAlaSerProTh 374

1167 CAACAGCTGCCAAGACTCC....ACGGACACCGAGAGCAACAACGAGGAGC 1213
     :|||::|||||||||||     |||||||||||||||||::::::
 374 rAsnGlyCysGlnAspSerAsnThrAspThrGluSerAsnHisGluGluA 391

1214 AGCGGCAGCGGGTCTTATCTACCTGACCAACCACCATCGCCGACGGCGCGCAA 1263
     ::  :::||               :: |||   :::
 391 rgGlySer.........................GlnAlaThrSerArgGlnSer 401

1264 CGGCGTGTCGCTCAAGGAGGAGCACCGCGCTACGAC.........CTGCT 1304
     ::  :::|||          |||::        :::
 402 SerAlaTyrAlaLysGluAspGlnArgProSerAspGlyLeuLeuLe 418

1305 G......CGCGCCGCCTCCGAGAACTCGCAGGACGGCCTCCGGTGTCA 1348
            :|||::||||||||          :::||||||||||::::::
 418 uProSerArgSerMetProGlyThrAlaLysSerLeuArgValLeuG 435

1349 GCACCAGCCGGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCGGGTG 1398
     ::  :::|||          ||||||||||||::: :::
 435 lyGluAspGlyValGlnValLysValPheLysCysGluHisCysArgVal 451

1399 CTCTTCCTGGATCACGTCATGTACACCATCCACATGGCGTTCGCGCACGGCTT 1448
     ||||||||||||||||::||||||||||||||||||||||||||||||
 452 LeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisGlyG1 468

1449 CCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCAGGACCGGT 1498
     ||||||||::|||||||||||||||||||||::|||||||||||
 468 uArgAspProPheGluCysAsnIleCysGlyTyrHisCysGlnAspArgT 485

1499 ACGAGTTCTGTGCGCACATAACGCGAGGGGAGCACCGC 1536
     ||||||||||::::||||||||||||
 485 yrGluPheSerHisIleValArgGlyHisLys 497
```

us-08-711-417c-165.rapn